

1/13

TTGAAATTATCTGGTCACTGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGTCTGA  
GGCGGGTGGACCACCTGGGGTCAGGAGTTTCGAGACCAGGCTGGCCAACATGGCGAAACCTGACTACA  
CAAAAAACACAAAATTTAGCCGGGGCTTGGGCGCTCCTGTGCTCCCAGCTACTCAGGAGGCTGAGGTG  
GGAGGACTGCTTGAGCCTGGGAGGTGAGGCTGCAGTGAGCTGTGATCGCGCCACTTAACTCCAGCC  
TGGACGACAGTGAGACCCTGTCTCAAGAAGAAAAAAGAAAGAAAGAAAAAAGAAAAAAGAA  
AATTATTTGGTCAATTATATGGTCAGCTCCCTCCACCACTCGCGAATTTACAGAAGAGGAGAAGTGGG  
CTGGGCGAGACCAGGACTAGCCCAAGATTACACAAGTTACTCGGTTGTAGAGCCAGGATTAGACAGGA  
GAGGCTCTAGATTCTGGTCTAGACTCCCCTCCTATTATTTAGCATTATGGCTTCCTGAGGATTACCAT  
GAGCCCTCCTCCACCGTCAAGCGGCAGCTACCAGCCACCAGACCAGATCCCTTCGAAGGTGCCCGGAG  
TACCAGACTGACAAAAGCGCCCGTACAGTGCTCAGTCCTGTAACCAAAGCTGTCTAGGGTGCAGACAT  
CGCTCACCGGACCGGGTAGGGCTCGTGCGCTAAGGGCGCCGGGTATTCCAGTTAGTGGAGAGGGAAGC  
GCCCTGGAAGTGCATGGGCCCCGGGAGAGGGCGCGGGAGCGGAGCATGGCCGGGCGGGGCGGGCCGCG  
GCCGTGGGCGGAGACTGCGCGCAGCTAGCTCGGGAGCGCCTCGGAGCC QCCCCGAGAGCCGCTTCT  
CGCGCCCCGAGCGCAGCGCAGCGCTCCGCCGTCTGACCTGCCGCGCCCGCAGCGTGCGGGCTGGGAA  
AGGAGGCGCTCACCGAGAGGGACCACGCGCCAGGCTCCAGCCCGACCCGGGACGCGGCGGGCGCGCG  
GAGCACCCATGGGCAGCCCCTGGAACGGCAGCGACGGCCCCGAGGGGGCGCGGGAGCCGCGCTGGCCC  
GCGCTGCCGCTTGCGACGAGCGCCGCTGCTCGCCCTTTCCCTGGGGGCGCTGGTGCCGGTGACCGC  
TGTGTGCTGTGCTGTTCTGTCGTGCGGGTGAGCGGCAACGTGGTGACCGTGATGCTGATCGGGCGCT  
ACCGGGACATGCGGACCACCACTTGTACCTGGGCAGCATGGCCGTGTCCGACCTACTCATCTG  
CTCGGGCTGCCGTTTCGACCTGTACCGCTCTGGCGCTCGCGGCCCTGGGTGTTCCGGGCCGCTGCTCTG  
CCGCTGTCCCTCTACGTGGGCGAGGGCTGCACCTACGCCACGCTGCTGCACATGACCGCGCTCAGCG  
TCGAGCGCTACCTGGCCATCTGCCGCCCGCTCCGCGCCCGCGTCTTGGTCACCCGGGCGCCGCTCCGC  
GCGCTCATCGCTGTGCTCTGGGCCGTGGCGCTGCTCTCTGCCGGTCCCTTCTTGTTCTTGGTGGGCGT  
CGAGCAGGACCCCGGCATCTCCGTAGTCCCGGGCTCAATGGCACCGCGCGGATCGCTCCTCGCCTC  
TCGCCTCGTCGCCGCTCTCTGGCTCTCGCGGGCGCCACCGCCGTCCCCGCCGTGGGGGCCGAGACC  
GCGGAGGCCGCGGCGCTGTTTCAGCCGCGAATGCCGGCCGAGCCCCGCGCAGCTGGGCGCGCTGCGTGT  
CATGCTGTGGGTACCAACCGCTACTTCTTCTGCCCTTCTGTGCTCAGCATCTCTACGGGCTCA  
TCGGGCGGGAGCTGTGGAGCAGCCGGCGGCCGCTGCGAGGCCGGCCGCTCGGGGCGGGAGAGAGGC  
CACCGGCAGACCGTCCGCGTCTGCgtaagtggagccgctggttccaaagacgcctgcctgcagtc  
cgccccgcggggaccgcgcaaagcctccctcccttcccttgcctgcgccagctctggtgcgcgcttc  
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cctgtccccccaggagctctggtgggaccccagggcgctttgaggtgggatccccggatccgattcagt  
aaccagcagtgcttttccagagcctctgagaccagaaaggagagttggttaattcttaaccaaccacc  
tgtagatgccacaaatgaggagtcctcacagtgctcttgagaagacgagggagatttcattaagcta  
aaatTTTTtatttaagttaagtgtgtaaggctaaagtaaacttgctcgatatcaaaaagtaaag  
attgtgcagacctgtttagaattcttttcaacagagaacagaaaacttgcttccgaagtgggtttgt  
ggaaggaagcctgccaaaggcgcttgttcagagaaattgctccttctggtttatgtccagccttgata  
acacatatgggagcctactatgcagttttaagcaagtatccatgcagcctgcagcctgggtcattttt  
tctggggtagagatctgcctaggtagaagtttctctaattttattttgctgttacttggtattgcaga  
tggttccttgtcggggtagggggtttatttgcttcccaatgcttttggttaatcccggtgctgtgtctt  
atgttgtagTGGTGGTGGTCTGGCATTATAATTTGCTGGTTGCCCTTCACGTTGGCAGAATCATT  
TACATAAACACGGAAGATTTCGCGGATGATGTACTTCTCTCAGTACTTTAACATCGTCGCTCTGCACT  
TTTCTATCTGAGCGCATCTATCAACCAATCCTCTACAACCTCATTTCAAAGAAGTACAGAGCGGCGG  
CCTTTAACTGCTGCTCGCAAGGAAGTCCAGGCCGAGAGGCTTCCACAGAAGCAGGGACACTGCGGGG  
GAAGTTGCAGGGGACACTGGAGGAGACACGGTGGGCTACACCGAGACAAGCGCTAACGTGAAGACGAT  
GGGATAA

FIG. 1

2/13

ATGGGCAGCCCTGGAACGGCAGCGACGGCCCCGAGGGGGCGCGGGAGCCGCGTGGCCCCGCGCTG  
CCGCCTTGCGACGAGCGCCGCTGCTCGCCCTTTCCCCTGGGGGCGCTGGTGCCGGTGACCGCTGTG  
TGCCTGTGCCTGTTCTGTCGTCGGGGTGAGCGGCAACGTGGTGACCGTGATGCTGATCGGGCGCTAC  
CGGGACATGCGGACCACCACCAACTTGTACCTGGGCAGCATGGCCGTGTCCGACCTACTCATCTG  
CTCGGGCTGCCGTTTCGACCTGTACCGCCTCTGGCGCTCGCGGCCCTGGGTGTTGGGGCCGCTGCTC  
TGCCGCCTGTCCCTCTACGTGGGCGAGGGCTGCACCTACGCCACGCTGCTGCACATGACCGCGCTC  
AGCGTCGAGCGCTACCTGGCCATCTGCCGCCCGCTCCGCGCCCGCGTCTTGGTCACCCGGCGCCGC  
GTCCGCGCGCTCATCGCTGTGCTCTGGGCCGTGGCGCTGCTCTCTGCCGGTCCCTTCTTGTTCCCTG  
GTGGGCGTCGAGCAGGACCCCGGCATCTCCGTAGTCCCGGGCCTCAATGGCACC GCGCGGATCGCC  
TCCTCGCCTCTCGCCTCGTCGCCCGCTCTCTGGCTCTCGCGGGCGCCACCGCCGTCCCCGCCGTCG  
GGGCCCCGAGACCGCGGAGGCCGCGGCGCTGTTCAAGCGGAATGCCGGCCGAGCCCCGCGCAGCTG  
GGCGCGCTGCGTGTCATGCTGTGGGTCAACACCGCCTACTTCTTCTGCCCTTTCTGTGCCTCAGC  
ATCCTCTACGGGCTCATCGGGCGGGAGCTGTGGAGCAGCCGGCGGCCGCTGCGAGGCCCGGCCGCC  
TCGGGGCGGGAGAGAGGCCACCGGCAGACCGTCCGCGTCTGCTGGTGGTGGTTCTGGCATTATA  
ATTTGCTGGTTGCCCTTCCACGTTGGCAGAATCATTTACATAAACACGGAAGATTCGCGGATGATG  
TACTTCTCTCAGTACTTTAACATCGTCGCTCTGCAACTTTTCTATCTGAGCGCATCTATCAACCCA  
ATCCTCTACAACCTCATTTCAAAGAAGTACAGAGCGGCGGCCTTAACTGCTGCTCGCAAGGAAG  
TCCAGGCCGAGAGGCTTCCACAGAAGCAGGGACACTGCGGGGGAAGTTGCAGGGGACACTGGAGGA  
GACACGGTGGGCTACACCGAGACAAGCGCTAACGTGAAGACGATGGGATAA

FIG.2

3/13

MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFPLGALVPVTAVCLCLFVVGVSNGNVVTVMLIGRY  
RDMRTTTNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPLLCLSLYVGEGETYATLLHMTAL  
SVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVEQDPGISVVPGLNGTARIA  
SSPLASSPPLWLSRAPPPSPPSGPETAEEAALFSRECRPSPAQLGALRVMLWVTTAYFFLPFLCLS  
ILYGLIGRELWSSRRPLRGPAASGRERGHRTVRVLLVVVLAFIICWLPFHVGRIIYINTEDSRMM  
YFSQYFNIVALQLFYLSASINPILYNLISKXYRAAAFLLLLARKSRPRGFHRSRDTAGEVAGDTGG  
DTVGYTETSANVKTMG

FIG.3

4/13

ATGGGCAGCCCCTGGAACGGCAGCGACGGCCCCGAGGGGGCGCGGGAGCCGCGTGGCCCCGCGCTG  
CCGCCTTGCGACGAGCGCCGCTGCTCGCCCTTTCCCTGGG&GCGCTGGTGCCGGTGACCGCTGTG  
TGCCTGTGCCTGTTTCGTCGTGCGGGTGAGCGGCAACGTGGTGACCGTGATGCTGATCGGGCGCTAC  
CGGGACATGCGGACCACCACCACTTGTACCTGGGCAGCATGGCCGTGTCCGACCTACTCATCCTG  
CTCGGGCTGCCGTTTCGACCTGTACCGCCTCTGGCGCTCGCGGCCCTGGGTGTTGCGGGCCGCTGCTC  
TGCCGCCTGTCCCTCTACGTGGGCGAGGGCTGCACCTACGCCACGCTGCTGCACATGACCGCGCTC  
AGCGTCGAGCGCTACCTGGCCATCTGCCGCCCCGCTCCGCGCCCGCTCTTGGTCACCCGGCGCCGC  
GTCCGCGCGCTCATCGCTGTGCTCTGGGCGGTGGCGCTGCTCTCTGCCGGTCCCTTCTTGTTCCCTG  
GTGGGCGTCGAGCAGGACCCCGGCATCTCCGTAGTCCCGGGCCTCAATGGCACCGCGCGGATCGCC  
TCCTCGCCTCTCGCCTCGTCGCCGCTCTCTGGCTCTCGCGGGCGCCACCGCCGTCCCCGCCGTGCG  
GGGCCCCGAGACCGCGGAGGCCGCGGCGCTGTTAGCCGCGAATGCCGGCCGAGCCCCGCGCAGCTG  
GGCGCGCTGCGTGTCATGCTGTGGGTACCAACCGCCTACTTCTTCTGCCCTTTCTGTGCCTCAGC  
ATCCTCTACGGGCTCATCGGGCGGGAGCTGTGGAGCAGCCGGCGGCCGCTGCGAGGCCCGGCCGCC  
TCGGGGCGGGAGAGAGAGGCCACCGGCAGACCGTCCGCGTCTGCGTAAGTGGAGCCGCCGTGGTTCC  
AAAGACGCCTGCCTGCAGTCCGCCCCGCCGGGGACCGCGCAAACGCTGGGTCCCTTCCCCTGCTC  
GCCCAGCTCTGGGCGCCGCTTCCAGCTCCCTTTCTATTTGATTCCAGCCTCCACCCGCCGTGGT  
GGTGGTTCTGGCATTATAATTTGCTGGTTGCCCTTCCACGTTGGCAGAATCATTTACATAAACAC  
GGAAGATTGCGGATGATGTACTTCTCTCAGTACTTTAACATCGTCGCTCTGCAACTTTTCTATCT  
GAGCGCATCTATCAACCAATCCTCTACAACCTCATTTCAAAGAAGTACAGAGCGGCGGCCTTTAA  
ACTGCTGCTCGCAAGGAAGTCCAGGCCGAGAGGCTTCCACAGAAGCAGGGACACTGCGGGGGAAGT  
TGCAGGGGACACTGGAGGAGACACGGTGGGCTACACCGAGACAAGCGCTAACGTGAAGACGATGGG  
ATAA

FIG.4

5/13

MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFPLGALVPVTAVCLCLFVVGVSIGNVIVMLIGRY  
RDMRTTTLNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPLLCLSLYVGEGETYATLLHMTAL  
SVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVEQDPGISVVPGLNGTARIA  
SSPLASSPPLWLSRAPPPSPPSGPETAEEAALFSRECRPSPAQLGALRVMLWTTAYFFLPFLCLS  
ILYGLIGRELWSSRRPLRGPAASGREGRGHRQTVRVLRKWSRRGSKDACLOSAPPGTAQTLGPLPLL  
AQLWAPLPAPFPISIPASTRRGGGSGIYNLLVALPRWQNHLLHKHGRFADDVLLSVL

FIG.5

FIG. 6A

7/13

(Donor A)  
CgtAAGTGGAGCCGCGTGGTTCCAAAGACGCTGCCTGCAGTCCGCCCGCCGGGACCGCGCAACGCTGGGTCCCT  
TCCCCTGCTGCCCCAGCTCTGGGCGCGCTTCCAGCTCCCTTTCCTATTTCGATTCCAGCTCCACCCGCCGgt...+569 bp  
(Donor B)

FM-1A: 7TM, 403 amino acids

IM6  
ag/CTG GTG GTG GTT CTG GCA TTT ATA ATT TGC TGG TTG CCC TTC CAC GTT GGC AGA ATC  
L V V V L A F I I C W L P F H V O R I  
IM7  
ATT TAC ATA AAC ACG GAA GAT TCG CGG ATG ATG TAC TTC TCT CAG TAC TTT AAC ATC GTC GCT CTG CAA CTT TTC  
I Y I N T E D S R M Y F S Q Y F N I V A L Q L F  
TAT CTG AGC GCA TCT ATC AAC CCA ATC CTC TAC AAC CTC ATT TCA AAG AAG TAC AGA GCG GCG GCC TTT AAA CTG  
Y L S A S I N P I L Y N L I S K K Y R A A A F K L  
CTG CTC GCA AGG AAG TCC AGG CCG AGA GGC TTC CAC AGA AGC AGG GAC ACT GCG GGG GAA GTT GCA GGG GAC ACT  
L L A R K S R P R G F H R S R D T A G E V A G D T  
GGA GGA GAC ACG GTG GGC TAC ACC GAG ACA AGC GCT AAC GTG AAG ACG ATG GGA TAA  
G G D T V G Y T E T S A N V K T M G \*

403

FIG.6B

FM-1B: 5TM, 387 amino acids

CGT AAG TGG AGC CGC CGT GGT TCC AAA GAC GCC TGC CTG CAG TCC GCC CCG GGG ACC GCG CAA ACG CTG  
R K W S R R G S K D A C L Q S A P P G T A Q T L

GGT CCC CTT CCC CTG CTC GCC CAG CTC TGG GCG CCG CTT CCA GCT CCC TTT CCT ATT TCG ATT CCA GCC TCC ACC  
G P L P L L A Q L W A P L P A P F P I S I P A S T

CGC CGT GGT GGT TCT GGC ATT TAT AAT TTG CTG GTT GCC CTT CCA CGT TGG CAG AAT CAT TTA CAT AAA CAC  
R R G G S G I Y N L L V A L P R W Q N H L H K H

GGA AGA TTC GCG GAT GAT GTA CTT CTC TCA GTA CTT TAA  
G R F A D D V L L S V L \*

387

FIG.6C



9/13

ATGCCCTGGACCAGACCCCAGGTGGACCTCCATGCTGCTGCAGCAGAGACCATGGACCAGTACACC  
ACGGACGACCACCACTACGAGGGCTCCCTCTTCCCCGCGTCCACCCTCATCCCCGTACGGTCATC  
TGCATCCTCATCTTCGTGGTCGGCGTGACCGGCAACACCATGACCATCCTCATCATCCAGTACTTC  
AAGGACATGAAGACCACCACCAACCTGTACCTGTCCAGCATGGCCGTGTCCGACCTCGTCATCTTC  
CTCTGCCTGCCCTTCGACCTGTACCGCCTGTGGAAGTACGTGCCGTGGCTGTTCCGGCAGGGCCGTG  
TGCCGCCTCTACCACTACATCTTCGAAGGCTGCACGTGCGCCACCATCCTCCACATCACGGCCCTG  
AGCATCGAGCGCTACCTGGCCATCAGCTTCCCCCTCAGGAGCAAGGTGATGGTGACCAGGAGAAGG  
GTCCAGTACATCATCCTGGCCCTGTGGTGCTTCGCCCTGGTGTCGGCCGCTCCACGCTCTTCCTG  
GTCGGGGTGGAGTACGACAACGAGACGCACCCCGACTACAACACGGGCCAGTGCAAGCACACGGGC  
TACGCCATCAGCTCGGGGCAGCTGCACATCATGATCTGGGTGTCCACCACCTACTTCTTCTGCCCG  
ATGCTGTGTCTCCTCTTCCTCTACGGCTCCATCGGGTGCAAGCTGTGGAAGAGCAAGAACGACCTG  
CAGGGCCCCTGCGCCCTGGCCCGCAGAGGTGCGCACAGGCAAACGGTGAAGATCCTGGTGGTGGTG  
GTGCTGGCCTTCATCATCTGCTGGCTGCCCTACCACATCGGCAGGAACCTGTTGCCCAGGTGGAC  
GACTACGACACGGCCATGCTCAGCCAGAATTTCAACATGGCCTCCATGGTGCTCTGCTACCTCAGC  
GCCTCCATCAACCCCGTCGTCTACAACCTGATGTCGAGGAAGTACCGGGCCGCCGCAAGCGCCTC  
TTCCTGCTCCACCAGAGACCCAAGCCGGCCACCGGGGCGAGGGGCAGTTTTCATGATCGGCCAC  
AGCCCCACCCTGGACGAGAGCCTGACGGGGGTGTGA

FIG.7

10/13

MPWTRPQVDLHAAAAETMDQYTTDDHHYEGSLFPASTLIPVTVICILIF W GVTGNT  
MTILIIQYFKDMKTTTNLYLSSMAVSDLVIFLCLPFDLYRLWKYVPWLFGEAVCRLY  
HYIFEGCTSATILHITALSIERYLAISFPLRSKVMVTRRRVQYIILALWCFALVSAA  
PTLFLVGVEYDNETHPDYNTGQCKHTGYAISSGQLHIMIWVSTTYFFCPMLCLFLY  
GSIGCKLWKSKNLQGPCALARERSHRQTVKILVVVVLAFIICWLPHYHGRNLFAQV  
DDYDTAMLSQNFNMAVMVLCYLSASINPVVYNLMSRKYRAAAKRLFLLHQRPKPAHR  
GQGQFCMIGHSPTLDESLTGV

FIG.8

11/13

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pu75E7 1 ..MPWTRPQVDLHAAAAETMDQYTTDDHHYEGSLFPASTLIPVTVICILI 48
      ||      |      ||      ||      ||      ||      ||      ||
huMTLR 1 MGSPWNGS..DGPEGAREPPWPALPPCDERRCSPFPLGALVPVTAVCLCL 48

      49 FVVGVTGNTMTILIIQYFKDMKTTTNLYLSSMAVSDLVIFLCPLPFDLYRL 98
      |||||.||.:::|:::||||||| |||||. | |||||
      49 FVVGVSIGNVVTVMILIGRYDMRTTNLYLGSMASDLLILLGLPFDLYRL 98

      99 WKYVPWLFGEAVCRLYHYIFEGCTSATILHITALSIERYLAISFPLRSKV 148
      |: ||.||. ||| |: |||| ||: |||. ||||| |||.:|
      99 WRSRPWFVGPLLCRLSLYVGEGCTYATLLHMTALSVERYLAICRPLRARV 148

      149 MVTRRRVQYIILALWCFALVSAAPTFLVGV EYD..... 182
      :|||||. :| || ||. || | ||||| |
      149 LVTRRRVRALIAVLWAVALLSAGPFLFLVGV EQDPGISVVPGLNGTARIA 198

      183 .....NETHPDYNTGQCKHTGYAISS.....GQLHIM 209
      | .| .| :| | :|
      199 SSPLASSPPLWLSRAPPSPSPSGPETAEAAALFSRECRPSPAQLGALRVM 248

      210 IWVSTTYFFCPMLCLLFLYGSIGCKLWKSNDLQGPCALARERSHRQTVK 259
      :|||. | || | || | || | || | || | || | || | || | || |
      249 LWVTTAYFFLPFLCLSILYGLIGRELWSSRRPLRGPAASGRERGHRTVR 298

      260 ILVVVVLAFIICWLPYHIGRNLFAQVDDYDTAMLSQNFNMASMLCYLSA 309
      :|. ||||| ||||| :|| :| :| || ||. :| ||||
      299 VLLVVVLAFIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSA 348

      310 SINPVVYNIMSRRYRAAAKRLFLLHQ.RPKPAHRGQ...GQFCMIGHSP 355
      ||||: |||. |: ||||| :| | . ||: || . | :|
      349 SINPILYNLISKKYRAAAFKLLARKSRPRGFHRSRDTAGEVAGDTGGDT 398

      356 LDESLTGV..... 363
      . . |
      399 VGYTETSANVKTMG 412

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FIG.9

12/13

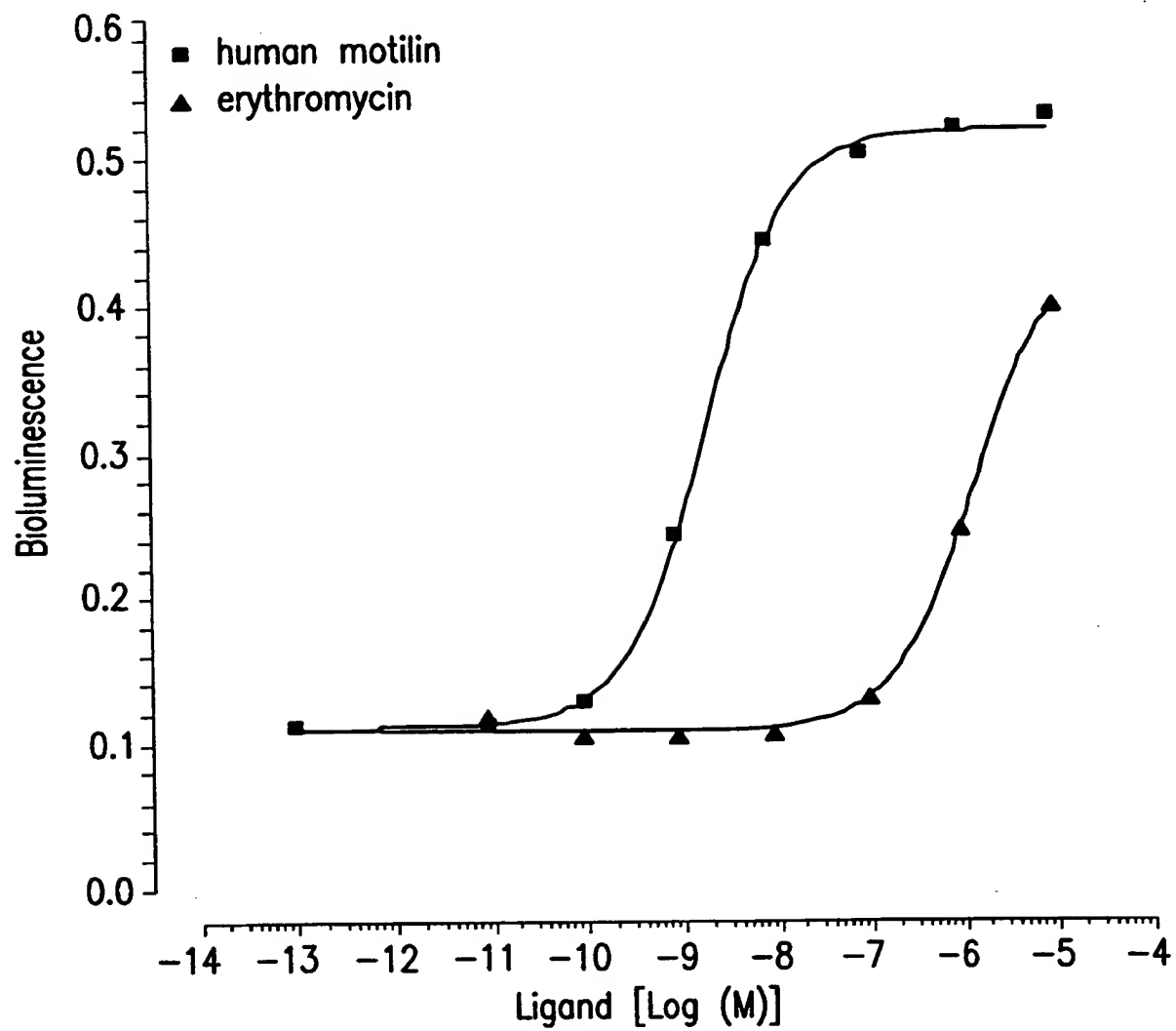


FIG.10

13/13

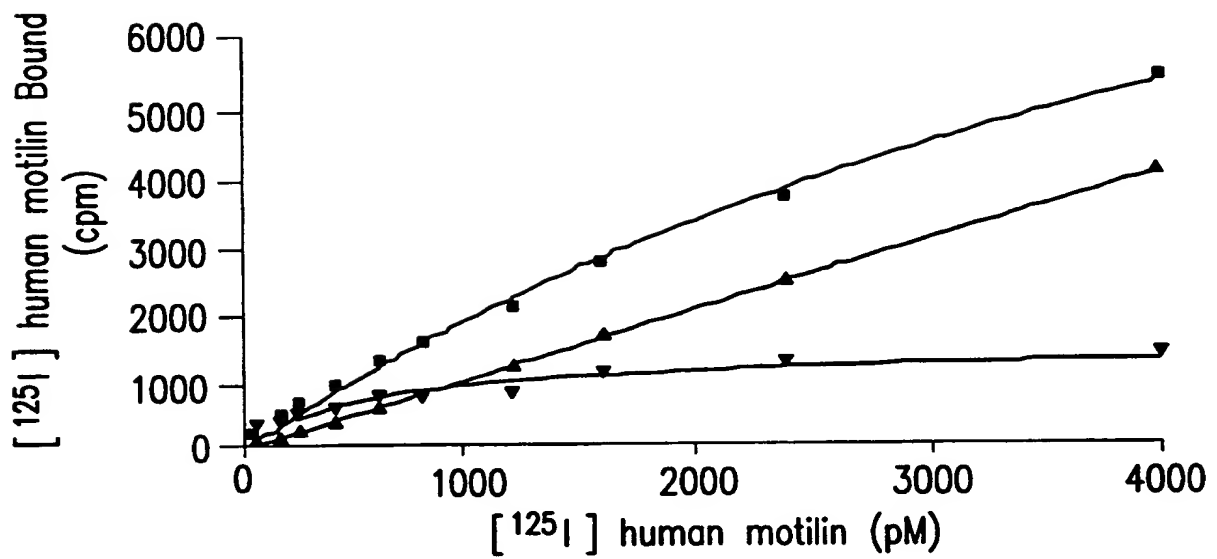


FIG. 11